Abstract of the Disclosure

During the structural analysis of a protein or peptide by tandem mass spectroscopy, a peptide ion derived from a protein that has already been measured and that is expressed in great quantities is avoided as a tandem mass spectroscopy target. A peptide derived from a minute amount of protein, which has heretofore been difficult to analyze, can be automatically determined as a tandem mass spectroscopy target within the real time of measurement. Data concerning a protein that has already been measured and a peptide derived from the protein is automatically stored in an internal database. The stored data is collated with measured data with high accuracy to determine an isotope peak. In this way, the process of selecting a peptide peak that has not been measured as the target for the next tandem analysis can be performed within the real time of measurement and a redundant measurement of peptides derived from the same protein can be avoided. The information contained in the MS^n spectrum is effectively utilized in each step of the MS^n involving a multi-stage dissociation and mass spectroscopy (MS^n), so that the flows for the determination of the next analysis content and the selection of the parent ion for the MS^{n+1} analysis, for example, can be optimized within the real time of measurement and with high efficiency and accuracy. Thus, a target of concern to the user can be subjected to tandem mass spectroscopy without wasteful measurement.